



1
SEQUENCE LISTING

pat
#10

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: The Government of the United States of America
as represented by the Secretary of the
Department of Health and Human Services

(B) STREET:

(C) CITY: Bethesda

(D) STATE: Maryland

(E) COUNTRY: USA

(F) POSTAL CODE (ZIP): 20892

(G) TELEPHONE: (301) 496-7056

(H) TELEFAX: (301) 402-0220

(I) TELEX:

(i) APPLICANT:

(A) NAME: Chandrasekharappa, Settara C.

(B) STREET: Laboratory of Gene Transfer
National Human Genome Research Institute
National Institute of Health

(C) CITY: Bethesda

(D) STATE: Maryland

(E) COUNTRY: USA

(F) POSTAL CODE (ZIP): 20892

(G) TELEPHONE:

(H) TELEFAX:

(I) TELEX:

(i) APPLICANT:

(A) NAME: Guru, Siradanahalli C.

(B) STREET: Laboratory of Gene Transfer
National Human Genome Research Institute
National Institute of Health

(C) CITY: Bethesda

(D) STATE: Maryland

(E) COUNTRY: USA

(F) POSTAL CODE (ZIP): 20892

(G) TELEPHONE:

(H) TELEFAX:

(I) TELEX:

(i) APPLICANT:

(A) NAME: Manickam, Pachiappan

(B) STREET: Laboratory of Gene Transfer
National Human Genome Research Institute
National Institute of Health

(C) CITY: Bethesda

(D) STATE: Maryland

(E) COUNTRY: USA

(F) POSTAL CODE (ZIP): 20892

(G) TELEPHONE:

(H) TELEFAX:

(I) TELEX:

B4

(i) APPLICANT:

- (A) NAME: Collins, Francis S.
- (B) STREET: Laboratory of Gene Transfer
National Human Genome Research Institute
National Institute of Health
- (C) CITY: Bethesda
- (D) STATE: Maryland
- (E) COUNTRY: USA
- (F) POSTAL CODE (ZIP): 20892
- (G) TELEPHONE:
- (H) TELEFAX:
- (I) TELEX:

(i) APPLICANT:

- (A) NAME: Emmert-Buck, Michael R.
- (B) STREET: Laboratory of Pathology
National Cancer Institute
National Institute of Health
- (C) CITY: Bethesda
- (D) STATE: Maryland
- (E) COUNTRY: USA
- (F) POSTAL CODE (ZIP): 20892
- (G) TELEPHONE:
- (H) TELEFAX:
- (I) TELEX:

(i) APPLICANT:

- (A) NAME: Debelenko, Larisa V.
- (B) STREET: Laboratory of Pathology
National Cancer Institute
National Institute of Health
- (C) CITY: Bethesda
- (D) STATE: Maryland
- (E) COUNTRY: USA
- (F) POSTAL CODE (ZIP): 20892
- (G) TELEPHONE:
- (H) TELEFAX:
- (I) TELEX:

(i) APPLICANT:

- (A) NAME: Lubensky, Irina A.
- (B) STREET: Laboratory of Pathology
National Cancer Institute
National Institute of Health
- (C) CITY: Bethesda
- (D) STATE: Maryland
- (E) COUNTRY: USA
- (F) POSTAL CODE (ZIP): 20892
- (G) TELEPHONE: (301) 496-7056
- (H) TELEFAX: (301) 402-0220
- (I) TELEX:

(i) APPLICANT:

(A) NAME: Liotta, Lance A.
(B) STREET: Laboratory of Pathology
National Cancer Institute
National Institute of Health

(C) CITY: Bethesda
(D) STATE: Maryland
(E) COUNTRY: USA
(F) POSTAL CODE (ZIP): 20892
(G) TELEPHONE: (301) 496-7056
(H) TELEFAX: (301) 402-0220
(I) TELEX:

(i) APPLICANT:

(A) NAME: Agarwal, Sunita K.
(B) STREET: Metabolic Diseases Branch
National Institute of Diabetes and Digestive
and Kidney Diseases
National Institute of Health

(C) CITY: Bethesda
(D) STATE: Maryland
(E) COUNTRY: USA
(F) POSTAL CODE (ZIP): 20892
(G) TELEPHONE:
(H) TELEFAX:
(I) TELEX:

(i) APPLICANT:

(A) NAME: Spiegel, Allen M.
(B) STREET: Metabolic Diseases Branch
National Institute of Diabetes and Digestive
and Kidney Diseases
National Institute of Health

(C) CITY: Bethesda
(D) STATE: Maryland
(E) COUNTRY: USA
(F) POSTAL CODE (ZIP): 20892
(G) TELEPHONE:
(H) TELEFAX:
(I) TELEX:

(i) APPLICANT:

(A) NAME: Burns, A. Lee
(B) STREET: Metabolic Diseases Branch
National Institute of Diabetes and Digestive
and Kidney Diseases
National Institute of Health

(C) CITY: Bethesda
(D) STATE: Maryland
(E) COUNTRY: USA
(F) POSTAL CODE (ZIP): 20892
(G) TELEPHONE:
(H) TELEFAX:
(I) TELEX:

- (i) APPLICANT:
- (A) NAME: Marx, Stephen J.
 - (B) STREET: Metabolic Diseases Branch
National Institute of Diabetes and Digestive
and Kidney Diseases
National Institute of Health
 - (C) CITY: Bethesda
 - (D) STATE: Maryland
 - (E) COUNTRY: USA
 - (F) POSTAL CODE (ZIP): 20892
 - (G) TELEPHONE:
 - (H) TELEFAX:
 - (I) TELEX:
- (i) APPLICANT:
- (A) NAME: Zhuang, Zhengping
 - (B) STREET: 9904 Pomona Drive
 - (C) CITY: Bethesda
 - (D) STATE: Maryland
 - (E) COUNTRY: USA
 - (F) POSTAL CODE (ZIP): 20892
 - (G) TELEPHONE:
 - (H) TELEFAX:
 - (I) TELEX:
- (ii) TITLE OF INVENTION: MEN1, the Gene Associated With Multiple
Endocrine Neoplasia Type 1, Menin Polypeptides, and Uses
Thereof
- (iii) NUMBER OF SEQUENCES: 28
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Townsend and Townsend and Crew LLP
 - (B) STREET: Two Embarcadero Center, Eighth Floor
 - (C) CITY: San Francisco
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94111-3834
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: US 09/380,337
 - (B) FILING DATE: 06-MAR-2000
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: US 60/040,269
 - (B) FILING DATE: 05-MAR-1997
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: WO PCT/US98/04258
 - (B) FILING DATE: 04-MAR-1998

- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Lockyer, Jean M.
 - (B) REGISTRATION NUMBER: 44,879
 - (C) REFERENCE/DOCKET NUMBER: 015280-315100US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (415) 576-0200
 - (B) TELEFAX: (415) 576-0300

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2772 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 111..1940
 - (D) OTHER INFORMATION: /product= "human menin"
- (ix) FEATURE:
 - (A) NAME/KEY: exon
 - (B) LOCATION: 1..87
- (ix) FEATURE:
 - (A) NAME/KEY: exon
 - (B) LOCATION: 88..555
- (ix) FEATURE:
 - (A) NAME/KEY: exon
 - (B) LOCATION: 556..764
- (ix) FEATURE:
 - (A) NAME/KEY: exon
 - (B) LOCATION: 765..893
- (ix) FEATURE:
 - (A) NAME/KEY: exon
 - (B) LOCATION: 894..934
- (ix) FEATURE:
 - (A) NAME/KEY: exon
 - (B) LOCATION: 935..1022
- (ix) FEATURE:
 - (A) NAME/KEY: exon
 - (B) LOCATION: 1023..1159
- (ix) FEATURE:
 - (A) NAME/KEY: exon
 - (B) LOCATION: 1160..1295
- (ix) FEATURE:
 - (A) NAME/KEY: exon
 - (B) LOCATION: 1296..1460

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION: 1461..2764

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGTGTCCGGA GCCGCGGACC TAGAGATCCC AGAAGCCACA GCGCAGCGGC CCGGCCCGCC	60
ACTATTTCCA GGCTCTGCGG GGCAGGGGCC GCCGCCACC GCCCGCCGCC ATG GGG	116
Met Gly	
1	
CTG AAG GCC GCC CAG AAG ACG CTG TTC CCG CTG CGC TCC ATC GAC GAC	164
Leu Lys Ala Ala Gln Lys Thr Leu Phe Pro Leu Arg Ser Ile Asp Asp	
5 10 15	
GTG GTG CGC CTG TTT GCT GCC GAG CTG GGC CGA GAG GAG CCG GAC CTG	212
Val Val Arg Leu Phe Ala Ala Glu Leu Gly Arg Glu Glu Pro Asp Leu	
20 25 30	
GTG CTC CTT TCC TTG GTG CTG GGC TTC GTG GAG CAT TTT CTG GCT GTC	260
Val Leu Leu Ser Leu Val Leu Gly Phe Val Glu His Phe Leu Ala Val	
35 40 45 50	
AAC CGC GTC ATC CCT ACC AAC GTT CCC GAG CTC ACC TTC CAG CCC AGC	308
Asn Arg Val Ile Pro Thr Asn Val Pro Glu Leu Thr Phe Gln Pro Ser	
55 60 65	
CCC GCC CCC GAC CCG CCT GGC GGC CTC ACC TAC TTT CCC GTG GCC GAC	356
Pro Ala Pro Asp Pro Pro Gly Gly Leu Thr Tyr Phe Pro Val Ala Asp	
70 75 80	
CTG TCT ATC ATC GCC GCC CTC TAT GCC CGC TTC ACC GCC CAG ATC CGA	404
Leu Ser Ile Ile Ala Ala Leu Tyr Ala Arg Phe Thr Ala Gln Ile Arg	
85 90 95	
GGC GCC GTC GAC CTG TCC CTC TAT CCT CGA GAA GGG GGT GTC TCC AGC	452
Gly Ala Val Asp Leu Ser Leu Tyr Pro Arg Glu Gly Gly Val Ser Ser	
100 105 110	
CGT GAG CTG GTG AAG AAG GTC TCC GAT GTC ATA TGG AAC AGC CTC AGC	500
Arg Glu Leu Val Lys Lys Val Ser Asp Val Ile Trp Asn Ser Leu Ser	
115 120 125 130	
CGC TCC TAC TTC AAG GAT CGG GCC CAC ATC CAG TCC CTC TTC AGC TTC	548
Arg Ser Tyr Phe Lys Asp Arg Ala His Ile Gln Ser Leu Phe Ser Phe	
135 140 145	
ATC ACA GGC ACC AAA TTG GAC AGC TCC GGT GTG GCC TTT GCT GTG GTT	596
Ile Thr Gly Thr Lys Leu Asp Ser Ser Gly Val Ala Phe Ala Val Val	
150 155 160	
GGG GCC TGC CAG GCC CTG GGT CTC CGG GAT GTC CAC CTC GCC CTG TCT	644
Gly Ala Cys Gln Ala Leu Gly Leu Arg Asp Val His Leu Ala Leu Ser	
165 170 175	
GAG GAT CAT GCC TGG GTA GTG TTT GGG CCC AAT GGG GAG CAG ACA GCT	692
Glu Asp His Ala Trp Val Val Phe Gly Pro Asn Gly Glu Gln Thr Ala	
180 185 190	

GAG Glu 195	GTC Val	ACC Thr	TGG Trp	CAC His	GGC Gly 200	AAG Lys	GGC Gly	AAC Asn	GAG Glu 205	GAC Asp 205	CGC Arg	AGG Arg	GGC Gly	CAG Gln 210	ACA Thr 210	740
GTC Val	AAT Asn	GCC Ala	GGT Gly 215	GTG Val 215	GCT Ala	GAG Glu	CGG Arg	AGC Ser	TGG Trp 220	CTG Leu 220	TAC Tyr	CTG Leu	AAA Lys 225	GGA Gly 225	TCA Ser 225	788
TAC Tyr	ATG Met	CGC Arg	TGT Cys 230	GAC Asp 230	CGC Arg	AAG Lys	ATG Met	GAG Glu 235	GTG Val 235	GCG Ala	TTC Phe	ATG Met	GTG Val 240	TGT Cys 240	GCC Ala 240	836
ATC Ile	AAC Asn 245	CCT Pro	TCC Ser	ATT Ile	GAC Asp	CTG Leu 250	CAC His	ACC Thr 250	GAC Asp	TCG Ser	CTG Leu 255	GAG Glu 255	CTT Leu	CTG Leu	CAG Gln	884
CTG Leu 260	CAG Gln 260	CAG Gln	AAG Lys	CTG Leu	CTC Leu	TGG Trp 265	CTG Leu	CTC Leu	TAT Tyr	GAC Asp 270	CTG Leu 270	GGA Gly	CAT His	CTG Leu	GAA Glu 270	932
AGG Arg 275	TAC Tyr	CCC Pro	ATG Met	GCC Ala 280	TTA Leu 280	GGG Gly	AAC Asn	CTG Leu	GCA Ala 285	GAT Asp 285	CTA Leu	GAG Glu	GAG Glu	CTG Leu	GAG Glu 290	980
CCC Pro	ACC Thr	CCT Pro	GGC Gly 295	CGG Arg	CCA Pro	GAC Asp	CCA Pro	CTC Leu	ACC Thr 300	CTC Leu	TAC Tyr	CAC His	AAG Lys	GGC Gly 305	ATT Ile 305	1028
GCC Ala	TCA Ser	GCC Ala 310	AAG Lys 310	ACC Thr	TAC Tyr	TAT Tyr	CGG Arg	GAT Asp 315	GAA Glu 315	CAC His	ATC Ile	TAC Tyr	CCC Pro 320	TAC Tyr	ATG Met 320	1076
TAC Tyr	CTG Leu 325	GCT Ala 325	GGC Gly 325	TAC Tyr	CAC His	TGT Cys	CGC Arg	AAC Asn 330	CGC Arg	AAT Asn 330	GTG Val 335	CGG Arg	GAA Glu 335	GCC Ala	CTG Leu 335	1124
CAG Gln 340	GCC Ala 340	TGG Trp	GCG Ala	GAC Asp	ACG Thr	GCC Ala 345	ACT Thr	GTC Val	ATC Ile	CAG Gln 350	GAC Asp 350	TAC Tyr	AAC Asn	TAC Tyr	TGC Cys 350	1172
CGG Arg 355	GAA Glu 355	GAC Asp	GAG Glu	GAG Glu	ATC Ile 360	TAC Tyr	AAG Lys	GAG Glu	TTC Phe	TTT Phe 365	GAA Glu 365	GTA Val	GCC Ala	AAT Asn	GAT Asp 370	1220
GTC Val	ATC Ile	CCC Pro	AAC Asn 375	CTG Leu 375	CTG Leu	AAG Lys	GAG Glu	GCA Ala 380	GCC Ala 380	AGC Ser	TTG Leu	CTG Leu	GAG Glu	GCG Ala 385	GGC Gly 385	1268
GAG Glu	GAG Glu	CGG Arg	CCG Pro 390	GGG Gly	GAG Glu	CAA Gln	AGC Ser	CAG Gln 395	GGC Gly	ACC Thr	CAG Gln	AGC Ser	CAA Gln 400	GGT Gly	TCC Ser 400	1316
GCC Ala	CTC Leu	CAG Gln 405	GAC Asp	CCT Pro	GAG Glu	TGC Cys	TTC Phe 410	GCC Ala 410	CAC His	CTG Leu	CTG Leu	CGA Arg 415	TTC Phe	TAC Tyr	GAC Asp 415	1364
GGC Gly 420	ATC Ile 420	TGC Cys	AAA Lys	TGG Trp	GAG Glu 425	GAG Glu	GGC Gly	AGT Ser	CCC Pro	ACG Thr	CCT Pro 430	GTG Val 430	CTG Leu	CAC His	GTG Val 430	1412

GGC TGG GCC ACC TTT CTT GTG CAG TCC CTA GGC CGT TTT GAG GGA CAG Gly Trp Ala Thr Phe Leu Val Gln Ser Leu Gly Arg Phe Glu Gly Gln 435 440 445 450	1460
GTG CGG CAG AAG GTG CGC ATA GTG AGC CGA GAG GCC GAG GCG GCC GAG Val Arg Gln Lys Val Arg Ile Val Ser Arg Glu Ala Glu Ala Ala Glu 455 460 465	1508
GCC GAG GAG CCG TGG GGC GAG GAA GCC CGG GAA GGC CGG CGG CGG GGC Ala Glu Glu Pro Trp Gly Glu Glu Ala Arg Glu Gly Arg Arg Arg Gly 470 475 480	1556
CCA CGG CGG GAG TCC AAG CCA GAG GAG CCC CCG CCG CCC AAG AAG CCA Pro Arg Arg Glu Ser Lys Pro Glu Glu Pro Pro Pro Pro Lys Lys Pro 485 490 495	1604
GCA CTG GAC AAG GGC CTG GGC ACC GGC CAG GGT GCA GTG TCA GGA CCC Ala Leu Asp Lys Gly Leu Gly Thr Gly Gln Gly Ala Val Ser Gly Pro 500 505 510	1652
CCC CGG AAG CCT CCT GGG ACT GTC GCT GGC ACA GCC CGA GGC CCT GAA Pro Arg Lys Pro Pro Gly Thr Val Ala Gly Thr Ala Arg Gly Pro Glu 515 520 525 530	1700
GGT GGC AGC ACG GCT CAG GTG CCA GCA CCC GCA GCA TCA CCA CCG CCG Gly Gly Ser Thr Ala Gln Val Pro Ala Pro Ala Ala Ser Pro Pro Pro 535 540 545	1748
GAG GGT CCA GTG CTC ACT TTC CAG AGT GAG AAG ATG AAG GGC ATG AAG Glu Gly Pro Val Leu Thr Phe Gln Ser Glu Lys Met Lys Gly Met Lys 550 555 560	1796
GAG CTG CTG GTG GCC ACC AAG ATC AAC TCG AGC GCC ATC AAG CTG CAA Glu Leu Leu Val Ala Thr Lys Ile Asn Ser Ser Ala Ile Lys Leu Gln 565 570 575	1844
CTC ACG GCA CAG TCG CAA GTG CAG ATG AAG AAG CAG AAA GTG TCC ACC Leu Thr Ala Gln Ser Gln Val Gln Met Lys Lys Gln Lys Val Ser Thr 580 585 590	1892
CCT AGT GAC TAC ACT CTG TCT TTC CTC AAG CGG CAG CGC AAA GGC CTC Pro Ser Asp Tyr Thr Leu Ser Phe Leu Lys Arg Gln Arg Lys Gly Leu 595 600 605 610	1940
TGAACTACTG GGGACTTCGG ACCGCTTGTTG GGGACCCAGG CTCCGCCTTA GTCCCCAAC	2000
TCTGAGCCCA TGTTCTGCCC CCAGCCCAA GGGGACAGGC CTCACCTCTA CCCAAACCCT	2060
AGGTTCCCGG TCCCGAGTAC AGTCTGTATC AAACCCACGA TTTTCTCCAG CTCAGAACCC	2120
AGGGCTCTGC CCCAGTCGTT AGAATATAGG TCTCTTCTCC CAGAATCCCA GCCGGCCAAT	2180
GGAAACCTCA CGCTGGGTCC TAATTACCAG TCTTTAAAGG CCCAGCCCCT AGAAACCCAA	2240
GCTCCTCCTC GGAACCGCTC ACCTAGAGCC AGACCAACGT TACTCAGGGC TCCTCCCAGC	2300
TTGTAGGAGC TGAGGTTTCA CCCTTAACCC AAGGGAGCAC AGGTCCCACC TCCAGCCCGG	2360
GGAGCCTAGG ACCACTCAGC CCCTAGGAGT ATATTTCCGC ACTTCAGAAT TCCATATCTT	2420
GCGAATCCAA GCTCCCTGCC CCAAATAACT TCAGTCCTGC TTCCAGAATT TGGAATCCT	2480


```

AGTTTCCTCT CCTTCGTATC CCGAGTCTGG GACACAAAAC TCCGCCCCCA GCCTATGAGC      2540
ATCCTGAGCC CCGCCCTCTT CCTGACGAAA CTGGCCCCCG ATCAGAGCAG GACCTCCCTT      2600
CCGACCCTCT GGGAACCTCC CAGAGGTCCA GCCCATCTCG GAGCATCCCG GAGGAAATCT      2660
GCAGAGGGGT TAGGAGTGGG TGACAAGAGC CTGATCTCTT CCTGTTTTGT ACATAGATTT      2720
ATTTTTTCAGT TCCAAGAAAG ATGAATACAT TTTGTTAAAA AAAAAAAAAA AA              2772

```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Met Gly Leu Lys Ala Ala Gln Lys Thr Leu Phe Pro Leu Arg Ser Ile
  1             5             10             15
Asp Asp Val Val Arg Leu Phe Ala Ala Glu Leu Gly Arg Glu Glu Pro
      20             25             30
Asp Leu Val Leu Leu Ser Leu Val Leu Gly Phe Val Glu His Phe Leu
      35             40             45
Ala Val Asn Arg Val Ile Pro Thr Asn Val Pro Glu Leu Thr Phe Gln
      50             55             60
Pro Ser Pro Ala Pro Asp Pro Pro Gly Gly Leu Thr Tyr Phe Pro Val
      65             70             75             80
Ala Asp Leu Ser Ile Ile Ala Ala Leu Tyr Ala Arg Phe Thr Ala Gln
      85             90             95
Ile Arg Gly Ala Val Asp Leu Ser Leu Tyr Pro Arg Glu Gly Gly Val
      100            105            110
Ser Ser Arg Glu Leu Val Lys Lys Val Ser Asp Val Ile Trp Asn Ser
      115            120            125
Leu Ser Arg Ser Tyr Phe Lys Asp Arg Ala His Ile Gln Ser Leu Phe
      130            135            140
Ser Phe Ile Thr Gly Thr Lys Leu Asp Ser Ser Gly Val Ala Phe Ala
      145            150            155            160
Val Val Gly Ala Cys Gln Ala Leu Gly Leu Arg Asp Val His Leu Ala
      165            170            175
Leu Ser Glu Asp His Ala Trp Val Val Phe Gly Pro Asn Gly Glu Gln
      180            185            190
Thr Ala Glu Val Thr Trp His Gly Lys Gly Asn Glu Asp Arg Arg Gly
      195            200            205

```

Gln Thr Val Asn Ala Gly Val Ala Glu Arg Ser Trp Leu Tyr Leu Lys
 210 215 220
 Gly Ser Tyr Met Arg Cys Asp Arg Lys Met Glu Val Ala Phe Met Val
 225 230 235 240
 Cys Ala Ile Asn Pro Ser Ile Asp Leu His Thr Asp Ser Leu Glu Leu
 245 250 255
 Leu Gln Leu Gln Gln Lys Leu Leu Trp Leu Leu Tyr Asp Leu Gly His
 260 265 270
 Leu Glu Arg Tyr Pro Met Ala Leu Gly Asn Leu Ala Asp Leu Glu Glu
 275 280 285
 Leu Glu Pro Thr Pro Gly Arg Pro Asp Pro Leu Thr Leu Tyr His Lys
 290 295 300
 Gly Ile Ala Ser Ala Lys Thr Tyr Tyr Arg Asp Glu His Ile Tyr Pro
 305 310 315 320
 Tyr Met Tyr Leu Ala Gly Tyr His Cys Arg Asn Arg Asn Val Arg Glu
 325 330 335
 Ala Leu Gln Ala Trp Ala Asp Thr Ala Thr Val Ile Gln Asp Tyr Asn
 340 345 350
 Tyr Cys Arg Glu Asp Glu Glu Ile Tyr Lys Glu Phe Phe Glu Val Ala
 355 360 365
 Asn Asp Val Ile Pro Asn Leu Leu Lys Glu Ala Ala Ser Leu Leu Glu
 370 375 380
 Ala Gly Glu Glu Arg Pro Gly Glu Gln Ser Gln Gly Thr Gln Ser Gln
 385 390 395 400
 Gly Ser Ala Leu Gln Asp Pro Glu Cys Phe Ala His Leu Leu Arg Phe
 405 410 415
 Tyr Asp Gly Ile Cys Lys Trp Glu Glu Gly Ser Pro Thr Pro Val Leu
 420 425 430
 His Val Gly Trp Ala Thr Phe Leu Val Gln Ser Leu Gly Arg Phe Glu
 435 440 445
 Gly Gln Val Arg Gln Lys Val Arg Ile Val Ser Arg Glu Ala Glu Ala
 450 455 460
 Ala Glu Ala Glu Glu Pro Trp Gly Glu Glu Ala Arg Glu Gly Arg Arg
 465 470 475 480
 Arg Gly Pro Arg Arg Glu Ser Lys Pro Glu Glu Pro Pro Pro Pro Lys
 485 490 495
 Lys Pro Ala Leu Asp Lys Gly Leu Gly Thr Gly Gln Gly Ala Val Ser
 500 505 510
 Gly Pro Pro Arg Lys Pro Pro Gly Thr Val Ala Gly Thr Ala Arg Gly
 515 520 525

Pro Glu Gly Gly Ser Thr Ala Gln Val Pro Ala Pro Ala Ala Ser Pro
 530 535 540
 Pro Pro Glu Gly Pro Val Leu Thr Phe Gln Ser Glu Lys Met Lys Gly
 545 550 555 560
 Met Lys Glu Leu Leu Val Ala Thr Lys Ile Asn Ser Ser Ala Ile Lys
 565 570 575
 Leu Gln Leu Thr Ala Gln Ser Gln Val Gln Met Lys Lys Gln Lys Val
 580 585 590
 Ser Thr Pro Ser Asp Tyr Thr Leu Ser Phe Leu Lys Arg Gln Arg Lys
 595 600 605
 Gly Leu
 610

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..9180
- (D) OTHER INFORMATION: /note= "genomic sequence for MEN1 gene"

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 1680..1766

(ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 1767..2264

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 2265..2732

(ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 2733..4296

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 4297..4505

(ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 4506..4715

(ix) FEATURE:
 (A) NAME/KEY: exon
 (B) LOCATION: 4716..4844

(ix) FEATURE:
 (A) NAME/KEY: intron
 (B) LOCATION: 4845..5176

(ix) FEATURE:
 (A) NAME/KEY: exon
 (B) LOCATION: 5177..5217

(ix) FEATURE:
 (A) NAME/KEY: intron
 (B) LOCATION: 5218..5297

(ix) FEATURE:
 (A) NAME/KEY: exon
 (B) LOCATION: 5298..5385

(ix) FEATURE:
 (A) NAME/KEY: intron
 (B) LOCATION: 5386..6024

(ix) FEATURE:
 (A) NAME/KEY: exon
 (B) LOCATION: 6025..6161

(ix) FEATURE:
 (A) NAME/KEY: intron
 (B) LOCATION: 6162..6622

(ix) FEATURE:
 (A) NAME/KEY: exon
 (B) LOCATION: 6623..6758

(ix) FEATURE:
 (A) NAME/KEY: intron
 (B) LOCATION: 6759..7195

(ix) FEATURE:
 (A) NAME/KEY: exon
 (B) LOCATION: 7196..7360

(ix) FEATURE:
 (A) NAME/KEY: intron
 (B) LOCATION: 7361..7577

(ix) FEATURE:
 (A) NAME/KEY: exon
 (B) LOCATION: 7578..8881

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGGTCTTGA ACTCCTGGCC TCAAGCAATC CTCCTGCTTC AGCTTCCCAA AGTGTTGTAA	60
TTACAGGCAT GAGCCTGGCA TGAAGTTGAC ACTATTGAGA TATACTGGTC AGGTATTTTG	120
TGGAATGTCC CTCAACTCTG TTTTGCCAGA TGTTTTCTCA TGATTAGAGG AGAGTTATAA	180

ATTTTGAGGA	AAATCCAGAG	AGGTGAAGAG	GTGAAGTAGG	GCAGAAATTT	AATCTGTTTT	240
ATTTACTGCT	ATATACCGAG	TGTCTGGAAC	TTGGCCCATG	GTAAGTACCA	AAAATCTGTT	300
TTTTTTGAAT	GAATAAGCAA	ATAAATGAGT	GACCGTGGA	ATTTAGTATT	ATTTCAAAGT	360
TTCAAAGCGT	TGTTGATACA	GGCCAGGCAC	AGTGGCTCAC	ACCTGTAATC	CCAGCACTTT	420
TGGAGGCCGA	GGTAGGAGGA	TCACTTGAGG	TCAGGAGTTC	GAGACCAGCC	TGACCAACAT	480
GGTGACACCC	CTGTCTCTAC	TAAGTAAAT	ACAAAAATTA	GCCAAGTGTG	GTGGCAGGCA	540
CCTGTAATCC	CGGCTACTTG	GGAAGCTGAG	GCAGAAGAAT	CACTTGAACC	TGGGAGGCAG	600
AGGTTGCAGT	GAGCCGAGAT	CACCCCACTG	CACTCCAGCC	TGAGTGACAG	AGCGAGACTC	660
TGTCTCAAAA	CAAATAAACA	AATAACTACT	CTTTGGCCGG	GTAAGGTGGT	TCACGCCTGT	720
AATTTTAGCA	CTTTGGGAGG	CTGAGGCGGG	CAGATCACTT	GAGGTTAGGG	GTTTCGAGACC	780
AGTCTGGCCA	ACATGGTGAA	ACCCCATCTC	TACTTAAAAT	ACAAAAAGTT	TTCTGGGTGT	840
GGTGGCGGAC	GCCTATAATC	CCAGCTACTT	GGGACTTTTT	TTTAAGACGG	AATCTCACTC	900
TGTTGCCAG	GCTGGAGTGC	AGTGGCAAGA	TTCTGGCTCA	CTGAAGCCTC	CGCCTCCAG	960
GTTCAAGGGG	ATTCCCCGCG	CCTCAGCCTC	CCAAGTAGCT	GGGAATCCCT	GTCTCTGCAA	1020
AAAAAAAAAA	AAAAAAAAAC	AAAAAATATA	TATATATATA	TATATGTGTG	TGTGTGTGTG	1080
TGTGTGTGTG	TTATATGTAT	ATATATTTAT	GTATATGCAC	ATACACACAA	AATTAGGCGG	1140
GAGTGGTGGC	GCACGCCTGT	GATCACAGCT	ACTCGGGAGG	CTGAGGCACG	AGAATCGCTT	1200
GAGCCCGTGA	AGTCGAGGCT	GCAGTGAGCC	CAGATCGAGC	CACTGCATTC	CAGCCTGGGC	1260
GAAAGAGAAA	GACCGTGTCT	CAAAACAAAC	AAACAAAAGC	TACTCTTAGC	ACGTGTTAGA	1320
GTATCTCGCG	GGCGGAAGTG	GGAAACGAGT	GCTGCACACA	GAGTAGGCAT	CTTTATATGT	1380
TAACAGACAC	TGATACCCAG	CTAAAGCGGC	TGAACACATT	TACTCTCTGG	CAGTGTTTAA	1440
AAGTATCTGT	TTTTCTCATA	TTGTTTTATT	TTAATTTTTT	CTGGATCAAG	CAACCTGATC	1500
TTTTTCCTCA	TAACTTGCCG	ACCGACCCGT	GACAGCAAAA	CCGGCAGAAG	CTCGGCGACC	1560
TCCCACCCCG	AGTCTGCAGG	TAGTGCCCCC	GGACTACATT	TTCCAGAAGG	CACTGCGGGC	1620
ACGCTTCCTG	CCTGGTCGGC	CTGAAGGGAA	GGGCCAATCC	CTGAGTATCT	CGGGAAGGAG	1680
GTGTCCGGAG	CCGCGGACCT	AGAGATCCCA	GAAGCCACAG	CGCAGCGGCC	CGGCCCCCCA	1740
CTATTTCCAG	GCTCTGCGGG	GCAGGGGTGG	GCCCAGACTC	CACTTCCCGG	CGGGTAGTGC	1800
GACCCTAGGG	GCGGGACTTC	ATGTCCCAGC	AGGCTCCGGG	CGGCGTGCGC	CGCGGTGCCT	1860
AGTGTGGGAT	GTAAGCGCGG	AGGTGGGCGA	GGGGGACCGA	GGCCAGGACT	CTCCTTGGGG	1920
TTTGGGGGCT	TGACCTGGGT	GCGCTTTCTG	GACAGACTTT	ACAGCCCCCG	GGGGCACAGT	1980
CGTAGAGAGG	GGGCGGGGCG	GCCATTGGGG	CTCCTCATTG	GGGTGCTTGG	GGCGCACCCC	2040

ATCGGGTACC	GGGCGTCCCG	GAATTGTGGG	GGACAAAAAG	GCTCTGCAGT	CTCGGCTGAG	2100
GGGTCTCACC	GACAAAAGAG	GGGAAGCCGG	TGAGCAGAGG	CTGAAGAGGG	TGGGGAAGCA	2160
GGGGAGCTGT	GCGTGTGTCTG	GGGCGGGTGG	AACCTTAGCG	GACCCTGGGA	GGAGGCTCCC	2220
CGGCCGAACC	TGCCCCACCC	TCCCTCCCCC	GGCTTGCCTT	GCAGGCCGCC	GCCCACCGCC	2280
CGCCGCCATG	GGGCTGAAGG	CCGCCCAGAA	GACGCTGTTC	CCGCTGCGCT	CCATCGACGA	2340
CGTGGTGCGC	CTGTTTGCTG	CCGAGCTGGG	CCGAGAGGAG	CCGGACCTGG	TGCTCCTTTC	2400
CTTGGTGCTG	GGCTTCGTGG	AGCATTTTCT	GGCTGTCAAC	CGCGTCATCC	CTACCAACGT	2460
TCCCAGAGTC	ACCTTCCAGC	CCAGCCCCGC	CCCCGACCCG	CCTGGCGGCC	TCACCTACTT	2520
TCCCGTGGCC	GACCTGTCTA	TCATCGCCGC	CCTCTATGCC	CGCTTCACCG	CCCAGATCCG	2580
AGGCGCCGTC	GACCTGTCCC	TCTATCCTCG	AGAAGGGGGT	GTCTCCAGCC	GTGAGCTGGT	2640
GAAGAAGGTC	TCCGATGTCA	TATGGAACAG	CCTCAGCCGC	TCCTACTTCA	AGGATCGGGC	2700
CCACATCCAG	TCCCTCTTCA	GCTTCATCAC	AGGTTGGAGC	CCAGTAGGTG	GGAATCTTAT	2760
CCATGACCCA	CTTCTTCAAA	ACCCTCCATG	GTTTACAGAA	CCCTTTTAAG	AACTGTAAGC	2820
CTTGTGAGGT	TCGGCAGGTG	TTATTTTCCT	CTTTGCAGTT	GGGAAACTGA	AGCCCAGAGA	2880
GGGGAAATGA	TATGCCAAAG	TCACACACGG	CATGGCAGGG	CTGGAAGTGA	AGCCTGATCA	2940
CTTGGCTCCA	AATCATCAAC	CTCACCTCTG	CCCCCTCAGC	ACCCCCACCC	TTGCCACTGA	3000
ACAGCTACAG	GAGTTCTAAG	CATGAGACAC	AGAGGGCGGC	AGCAGATTTA	GGGGGCAAGA	3060
AGATGAAATT	GGGCTGCATT	TGAGGCAGTT	AAACAAAATA	ATGGCTATGA	AGATTTTTTT	3120
TTTTTTTTTT	TTTGTAGACA	GGGTCTCACT	CTGTCCCCCA	GGCTGGAGTG	CAGTGGTGTG	3180
ATCATGGCTC	ACTGCAGCCT	CAGTCTCCCT	GGGCTCAGAG	ATCCTCCAAC	CTCAGCCTCC	3240
TGAGTAGCTG	AGAGTACAGG	CATGCACCGT	GGTGCTGGTT	AATTTTTTGT	ATTTTTTTTG	3300
TAGAGATGGT	GTCTCACTAT	GTGGCCCAGA	CTGGTCTTGA	ACTCTGGGGC	TCAAGTGATC	3360
TGCCCCGCTC	AGTCTCCCAA	ATGCTGGGAT	TACAGGTGTG	AGCCACCGCA	ACTGGTGGCC	3420
TATGAAAATT	TTTTTTTTTT	TTCAGACGGC	GTCTCACTCT	GTCGCCCAGG	CTGGAGTGCA	3480
GTGGTGCAAT	CTCGGCTCAC	TGCAAGCTCT	GCCTCCTGCT	TTCATGCCAT	TCTCCTGCCT	3540
CCTGCCTCAG	CCTCCTGAGT	AGCTGGGACT	ACAGGAGCCT	GCCACCATGC	CTGGCTAATT	3600
TTTTTTTTGGA	TTTTTAGTAG	AGACGAGGTT	TCACCATGTT	AGCCAGGATG	GTCTCGATCT	3660
CCTGACCTCG	TGATCCGCCC	GCCTTGGCCT	CCCAAAGTGC	TGGGATTACA	GGCGTGAGCC	3720
ACCGCACCTG	GTCAAAAATG	TTTGAGACAG	AGAAGGGGCT	TGACCTCAAA	AGGCTTAAGA	3780
GTCAGGGCTT	GCAAAGAGCT	TTGCACCAAG	CCCGGTTGAC	TGGCAATCCC	ATCCTGGTGT	3840
GCCATATTGA	GAAGGAATCA	GAGGCTGCTT	CTCAGCTTAG	CAGGAAAAGA	GTGCAGAGAT	3900

AAATGAGGGT	TATTTGTTGG	TGGGTGTATA	GCCAGAGAGT	GTTGGCCAGC	GTCCTGTTTT	3960
TGCCATTCCT	GTTTTAACCT	AGTAAGTGCA	GTAAATGGA	ATCCCTAAAT	CCATAGAATA	4020
TATAATAGAG	TTGCAGAGAA	AGACGAGGTA	GGGCCAAAGG	CTGGGTCAGC	TACAGGATAT	4080
CCAGAAAGGT	ATCTTGTTGG	ACATAGAGGG	TGTAAACAGG	GAGAGAGTCT	TTGAACACGT	4140
GGGAGGGAAG	GGATGGAGGG	ATAGTGGGCA	GGAGAATCTG	AGGTTGGGTC	ACAGGCTTGG	4200
AAAGGGAGTG	GGAGGGAGTG	TGGCCCATCA	CTACCTGGCC	CCTTTCCCCA	TGTTAAAGCA	4260
CAGAGGACCC	TCTTTCATTA	CCTCCCCCTT	CCACAGGCAC	CAAATTGGAC	AGCTCCGGTG	4320
TGGCCTTTGC	TGTGGTTGGG	GCCTGCCAGG	CCCTGGGTCT	CCGGGATGTC	CACCTCGCCC	4380
TGTCTGAGGA	TCATGCCTGG	GTAGTGTTTG	GGCCCAATGG	GGAGCAGACA	GCTGAGGTCA	4440
CCTGGCACGG	CAAGGGCAAC	GAGGACCGCA	GGGGCCAGAC	AGTCAATGCC	GGTGTGGCTG	4500
AGCGGGTATT	GTTCCCTCCC	CCCAGCCTTG	TCCCCTTCAT	ACTGTAGTAG	CCCAAGCCAC	4560
CCAAGGGACT	CCATTTTCTT	GGGCCACACC	CCTTTCTTCC	CATCACCACC	CACATAGGAA	4620
GGGAAGACAG	AAGAGCCCCT	TTTCCTGGCT	GTCATTCCCT	GAAGCAGGCA	CAGGGTGGGC	4680
CATCATGAGA	CATAATGATC	TCATCCCCCC	CTAAGAGCTG	GCTGTACCTG	AAAGGATCAT	4740
ACATGCGCTG	TGACCGCAAG	ATGGAGGTGG	CGTTCATGGT	GTGTGCCATC	AACCCTTCCA	4800
TTGACCTGCA	CACCGACTCG	CTGGAGCTTC	TGCAGCTGCA	GCAGGTGAGG	GCTGAGCCAA	4860
TGGGGCAGGA	CTGGGCTAGG	CCAGACTTGA	CTTGCTGTGG	GACCTGGGC	AGGGGCACTT	4920
TCCCTTCCTG	AGCTTCAGCT	TCCCTCCTG	GAAAAATGGG	TTAGTAATTC	CTGGCCTGGC	4980
CTTTCCAGG	GCTCTTGGGA	GAGTAGAATT	GAGATGTGAA	ATTGCTTTGA	CTCCATTAAA	5040
GGGCTGGTCC	CAGAATTTTG	GCCCTTCCAC	ATGGTGGGTG	GTCCCTGTTG	GTTCTGACCC	5100
CCACCTCTGC	CCGATAGGCT	AAGGACCGGT	TCTCCTCCCT	GTTCCGTGGC	TCATAACTCT	5160
CTCCTTCGGC	TCCTAGAAGC	TGCTCTGGCT	GCTCTATGAC	CTGGGACATC	TGGAAAGGTC	5220
AGTAGAGGGA	AGTGGCCAGG	CTGCGCCTGG	TGAGGCCGGG	GGGCTGGGTG	GCAGCCTGAA	5280
TTATGATCCT	TTCCTAGGTA	CCCCATGGCC	TTAGGGAACC	TGGCAGATCT	AGAGGAGCTG	5340
GAGCCCACCC	CTGGCCGGCC	AGACCCACTC	AGCCTCTACC	ACAAGGTGGG	GGCATCTAAG	5400
GAGGGTGCAG	AAGGGAGAGC	CTACAGTGG	CTGAGGCAGG	GGCCCTCATC	TGGGCAGATG	5460
AGAAGAGAAC	TTTGTGTGTT	GGGGGGTATC	GCCCATCCAG	TCTCACTTTG	TGTCAACTGT	5520
GTGCAGAATC	AGTTCAGTCA	GGGCTGTCTG	AGGGGTCTCC	AGGGTTCCCC	AGCCTGGGAG	5580
TGGCAGGGGC	TGCATTTGTC	CCCTCAGCCC	TGCCTTTTCT	GCCACTGCTT	ACTGTCCTTC	5640
CTGGAGTATA	ACAGAGGTCA	AATGTGGTAG	GAGCACTGAA	GAGGGGGTGT	TCACTTGGTG	5700
GGTGTAGGTG	GGGAGGAGGG	CCATTGGGCT	GGGCTTGAAA	GTCTTTGGTG	ATGTGTAGAA	5760

GAGTGTCTGA	GAAAGAGAAG	GGCCCTGAGC	TCGGAGGGCA	GGCCCCACCC	CTGCAGTCTG	5820
CCCCAGGCCT	CAGCCAGCAG	TCCTGTAGAC	CCAGGGAGGA	GACCAGGTAG	AAGGGCTGGC	5880
AGCGAGTGGA	GGTGGGAGTG	GAGATGGAGA	GGACTCCCTG	GGATCTTCCT	GTGGCCCCTT	5940
CTGGGTGTGC	CCTGGTGGGG	CATTTGTGCC	AGCAGGGCAG	CTGGGGCTGC	CTCCCTGAGG	6000
ATCCTCTGCC	TCACCTCCAT	CCAGGGCATT	GCCTCAGCCA	AGACCTACTA	TCGGGATGAA	6060
CACATCTACC	CCTACATGTA	CCTGGCTGGC	TACCACTGTC	GCAACCGCAA	TGTGCGGGAA	6120
GCCCTGCAGG	CCTGGGCGGA	CACGGCCACT	GTCATCCAGG	AGTGAGGATC	CCCCTACTAG	6180
GGCCTGCAGC	CTGTCCTTTC	TTCCCCTCCA	TCAGTTTCCA	ACCACCCTCG	TCCAGGACTG	6240
AGGCCTGGCT	CCCACGCCCC	ATCCCCTTTC	CATCCAGTCC	CTAGGCAGCA	AGGCCACCAT	6300
TACCCAGGAG	GTAGGGACCC	TGATTAAGGT	GTCACATCTT	TCCCTCCCTC	CCCTCTCCTC	6360
CTAATTTTTT	TTTTCTCAGA	ACAGTCTCAA	ATCTCCAATG	TTTAACCACC	ATCATCCAGC	6420
AGTGGGACTT	CCACCCTCGG	CCCCATGCCC	CCCTCCTCAT	TCTTGCTTTC	TTCTCTGGG	6480
CTGACCCAGA	CAGCATCATT	TTGCAGTGAG	GACCCACCT	ACTCCCCCAG	CCCCTGGGGG	6540
CTCCATCCCC	CGCCAGGTCC	CTGGGGCTAC	CCCCGATGGT	GAGACCCCTT	CAGACCCTAC	6600
AGAGACCCCA	CTGCTCTCAC	AGCTACAAC	ACTGCCGGGA	AGACGAGGAG	ATCTACAAGG	6660
AGTTCTTTGA	AGTAGCCAAT	GATGTCATCC	CCAACCTGCT	GAAGGAGGCA	GCCAGCTTGC	6720
TGGAGGCGGG	CGAGGAGCGG	CCGGGGGAGC	AAAGCCAGGT	GAAAGGCTGG	AGCTCCAGCC	6780
TGTGTCCAGC	CTCCCACCTG	GACAGGGCTC	CCTTCCACAG	GGCCATGGGG	GCTGCATGTA	6840
CGGGATTAGG	GATGGCAGGA	GGAAGGTGGC	CCTGAGCAGA	CAGCTATGTT	CCCTTTTGCT	6900
ATAACTGAGG	TCCTGGGCCC	ACGTTGGACG	GGACTGAAGG	TATTTTAGAG	GTTTCTACCC	6960
TGTGCCTTCA	GTTTCATGGC	CAGACTCCCT	CCCTCAGCTG	AGGGGTGGAG	GTAGGGATGG	7020
TACGTCCTGG	CTATGGATTG	GCTTTATAAA	AGGAAAGAGG	TTCTAAGAAT	GTTCCCAACC	7080
TATGCTTACC	TTTTCTGGAG	CCAGGGGTCT	TTGCCTAGGT	GGGGGGCCTG	GCCTGTGCCC	7140
TCTGCTAAGG	GGTGAGTAAG	AGACTGATCT	GTGCCCTCCC	TTCCCCCTCG	TCCAGGGCAC	7200
CCAGAGCCAA	GGTTCCGCCC	TCCAGGACCC	TGAGTGCTTC	GCCCACCTGC	TGCGATTCTA	7260
CGACGGCATC	TGCAAATGGG	AGGAGGGCAG	TCCCACGCCT	GTGCTGCACG	TGGGCTGGGC	7320
CACCTTTCTT	GTGCAGTCCC	TAGGCCGTTT	TGAGGGACAG	GTGAGGGACA	GCTGCACAGA	7380
GGTCTGGGCA	CTACAGGTGG	TGACAGCAGC	CACGGGCTTG	TCAGACTTTT	CTGGCCCAGG	7440
GGCAGCATCT	GCCCATCCCC	TTCGGTGCCG	ATGGGACTGA	GACCCCTGG	GTGGGATGGG	7500
ATGGCCAGAG	CAGGGTCCTG	GAGTTCCAGC	CACTGGCCGG	CAACCTTGCT	CTCACCTTGC	7560
TCTCCCCACT	GGCCCAGGTG	CGGCAGAAGG	TGCGCATAGT	GAGCCGAGAG	GCCGAGGCGG	7620

CCGAGGCCGA	GGAGCCGTGG	GGCGAGGAAG	CCCGGGAAGG	CCGGCGGCGG	GGCCCACGGC	7680
GGGAGTCCAA	GCCAGAGGAG	CCCCCGCCGC	CCAAGAAGCC	AGCACTGGAC	AAGGGCCTGG	7740
GCACCGGCCA	GGGTGCAGTG	TCAGGACCCC	CCCGGAAGCC	TCCTGGGACT	GTCGCTGGCA	7800
CAGCCCGAGG	CCCTGAAGGT	GGCAGCACGG	CTCAGGTGCC	AGCACCCGCA	GCATCACCAC	7860
CGCCGGAGGG	TCCAGTGCTC	ACTTTCCAGA	GTGAGAAGAT	GAAGGGCATG	AAGGAGCTGC	7920
TGGTGGCCAC	CAAGATCAAC	TCGAGCGCCA	TCAAGCTGCA	ACTCACGGCA	CAGTCGCAAG	7980
TGCAGATGAA	GAAGCAGAAA	GTGTCCACCC	CTAGTGACTA	CACTCTGTCT	TTCCTCAAGC	8040
GGCAGCGCAA	AGGCCTCTGA	ACTACTGGGG	ACTTCGGACC	GCTTGTGGGG	ACCCAGGCTC	8100
CGCCTTAGTC	CCCCAACTCT	GAGCCCATGT	TCTGCCCCCA	GCCCAAAGGG	GACAGGCCTC	8160
ACCTCTACCC	AAACCCTAGG	TTCCCGGTCC	CGAGTACAGT	CTGTATCAAA	CCCACGATTT	8220
TCTCCAGCTC	AGAACCCAGG	GCTCTGCCCC	AGTCGTTAGA	ATATAGGTCT	CTTCTCCAG	8280
AATCCCAGCC	GGCCAATGGA	AACCTCACGC	TGGGTCCTAA	TTACCAGTCT	TTAAAGGCCC	8340
AGCCCCTAGA	AACCCAAGCT	CCTCCTCGGA	ACCGCTCACC	TAGAGCCAGA	CCAACGTTAC	8400
TCAGGGCTCC	TCCCAGCTTG	TAGGAGCTGA	GGTTTCACCC	TTAACCCAAG	GGAGCACAGG	8460
TCCCACCTCC	AGCCCGGGGA	GCCTAGGACC	ACTCAGCCCC	TAGGAGTATA	TTCCGCACT	8520
TCAGAATTCC	ATATCTTGCG	AATCCAAGCT	CCCTGCCCCA	AATAACTTCA	GTCCTGCTTC	8580
CAGAATTTGG	AAATCCTAGT	TTCCTCTCCT	TCGTATCCCG	AGTCTGGGAC	ACAAACTCC	8640
GCCCCAGCC	TATGAGCATC	CTGAGCCCCG	CCCTCTTCCT	GACGAAACTG	GCCCCGGATC	8700
AGAGCAGGAC	CTCCCTTCCG	ACCCTCTGGG	AACCTCCCAG	AGGTCCAGCC	CATCTCGGAG	8760
CATCCCGGAG	GAAATCTGCA	GAGGGGTTAG	GAGTGGGTGA	CAAGAGCCTG	ATCTCTTCCT	8820
GTTTTGTACA	TAGATTTATT	TTTCAGTTCC	AAGAAAGATG	AATACATTTT	GTTAAAAAAA	8880
ATATAAAGCG	CAAGTCCATG	TTTATCTGGG	AAATTGGGGA	TGGGGCGGGG	AGTGGAGCGC	8940
CCCTTCTTCC	CTTTGTCTTC	TGGCTCCCGG	GACTTTGCGC	TCCCTACCTG	TGGAGCGCGA	9000
GCGACAGTGG	CGGCGGAAGG	ACGTAGGCTC	CGCCCCGGCC	TTGGGGCTTC	CCCCGCGCCG	9060
CCGAGGGCCC	GTCCCGCGGG	CGCCTCCTCC	CGGACTGGCG	GTGGGGCATC	CCNGGGCGCG	9120
GCCCCGCCCC	CGGGCTTCAG	CCCCGCCCCC	GCGGCTTCAG	AGCCACGGGC	GCCCGCCCCG	9180

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "antisense strand from patient with 512delC frameshift mutation"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GATCCTTAAG TAGGAGCGG

19

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "antisense strand from normal sequence (positions 500-519 of MEN1 cDNA)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATCCTTGAA GTAGGAGCGG

20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "antisense strand from normal sequence (positions 1405-1424 of MEN1 cDNA)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGTGGCCCAG CCCACGTGCA

20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "antisense strand from position
1417 C->T substitution, resulting in
W436X mutation"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGTGGCCTAG CCCACGTGCA

20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GACCTGGGTG CGCTTTCTGG AC

22

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTTGGACATA GAGGGTGTAACACAG

24

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGTGAGCTCG GGAACGTTGG TAG

23

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAGACCTTCT TCACCAGCTC ACGG

24

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGAACCTCAC AAGGCTTACA GTTC

24

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTTGGACATA GAGGGTGTAA ACAG

24

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ACAGTTGACA CAAAGTGAGA CTGG

24

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGCTCTTCTG TCTTCCCTTC CTATG

25

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGTCCCACAG CAAGTCAAGT CTGG

24

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCTGTTCCGT GGCTCATAAC TCTC

24

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCTCAGCCAG CAGTCCTGTA GA

22

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGACGAGGGT GGTGGAAAC TG

22

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGACTCCTTG GGATCTTCCT GTG

23

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AACGACCATC ATCCAGCAGT GG

22

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CCATCCCTAA TCCCGTACAT GC

22

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TGGTGAGACC CCTTCAGACC CTAC

24

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTGCTAAGGG GTGAGTAAGA GAC

23

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGTTTGATAC AGACTGTACT CGG

23

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTCTGACAAG CCCGTGGCTG CTG

23

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GCATCTGCCC ATCCCCTTCG GTG

23

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GAAGCCTCCT GGGACTGTCG CTG
